Figure 1

Heteractis crispa chromoprotein **wild type (base isoform)**

```
            10        20        30        40        50        60
 5'ACCATTTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGAACGAAAACTGACCCAAATTACA
            70        80        90       100       110       120
   TCTTCCTCCTGGATCCTTACCATGGCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATG
                         M  A  G  L  L  K  E  S  M  R  I  K  M
           130       140       150       160       170       180
   TACATGGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAAC
   Y  M  E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N
           190       200       210       220       230       240
   CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTT
   P  F  T  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F
           250       260       270       280       290       300
   GCCTTCGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACG
   A  F  D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T
           310       320       330       340       350       360
   GCAGAGATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACC
   A  E  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T
           370       380       390       400       410       420
   ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC
   T  T  Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N
           430       440       450       460       470       480
   TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATG
   C  L  I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M
           490       500       510       520       530       540
   AAGAACAAATCAGGAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGAGAATGGTGTC
   K  N  K  S  G  G  W  E  P  C  T  E  V  V  Y  P  E  N  G  V
           550       560       570       580       590       600
   CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC
   L  C  G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  L
           610       620       630       640       650       660
   TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTT
   Y  T  S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F
           670       680       690       700       710       720
   ACAGACATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAA
   T  D  I  R  L  Q  M  P  R  K  K  K  D  E  Y  F  E  L  Y  E
           730       740       750       760       770       780
   GCATCTGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGATTGTTCCCAGTGACA
   A  S  V  A  R  Y  S  D  L  P  E  K  A  N  *
           790       800       810       820       830       840
   CCAGACTGCTGTCAGCTTTTGGTTAAAGCCCGAAAGACAAAAGGACATTTGTAGTTTAGT
           850       860       870       880       890       900
   TTATATTTCCCTTTCATTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAAATGCTC
           910
   CATTAAACCT 3' (SEQ ID NOs: 01 & 02)
```

Figure 2

Heteractis crispa chromoprotein **wild type (second isoform)**

```
         10        20        30        40        50        60
5'ACCATTTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGACGAAAACTGACCCAAATTACAT

        70        80        90       100       110       120
CCTCCTGATCCTTACCATGGCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATGTACAT
                   M  A  G  L  L  K  E  S  M  R  I  K  M  Y  M

       130       140       150       160       170       180
GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
 E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N  P  F

       190       200       210       220       230       240
TACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
 T  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F  A  F

       250       260       270       280       290       300
CGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
 D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T  A  E

       310       320       330       340       350       360
GATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
 I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T  T  T

       370       380       390       400       410       420
CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
 Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N  C  L

       430       440       450       460       470       480
TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
 I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M  K  N

       490       500       510       520       530       540
CAAATCAGAAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGATAATGGTGTCCTGTG
 K  S  E  G  W  E  P  C  T  E  V  V  Y  P  D  N  G  V  L  C

       550       560       570       580       590       600
TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTCTATAC
 G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  L  Y  T

       610       620       630       640       650       660
TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA
 S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F  T  D

       670       680       690       700       710       720
CATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
 I  R  L  Q  M  P  R  K  K  K  D  E  Y  F  E  L  Y  E  A  S

       730       740       750       760       770       780
TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGATTGTTCCCAGTGACACCAGA
 V  A  R  Y  S  D  L  P  E  K  A  N  *

       790       800       810       820       830       840
CTGCTGTCAGCTTTTGGTTAAAGCCCGAAAGACAAAAGGACATTTGTAGTTTTAGTTTAT

       850       860       870       880       890       900
ATTTTCCCTTTCATTTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAAATGCTCCA

TTAAACCT 3' (SEQ ID NOs: 03 & 04)
```

Figure 3

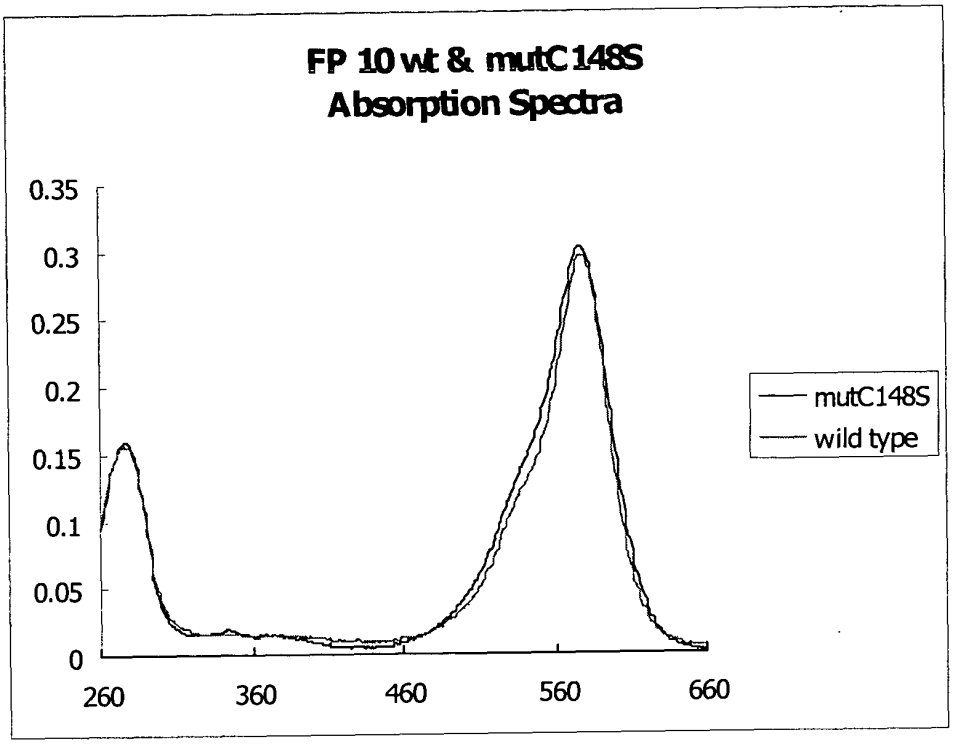

Figure 4

Heteractis crispa fluorescent protein **mutant C148S**

C148S according to GFP numbering
C143S according to self-numbering.

```
                                     ATGGCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATG
                                     M  A  G  L  L  K  E  S  M  R  I  K  M

TACATGGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAAC
Y  M  E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N

CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTT
P  F  T  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F

GCCTTCGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACG
A  F  D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T

GCAGAGATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACC
A  E  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T

ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC
T  T  Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N

TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATG
C  L  I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M

AAGAACAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTC
K  N  K  S  G  G  W  E  P  S  T  E  V  V  Y  P  E  N  G  V

CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC
L  C  G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  L

TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTT
Y  T  S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F

ACAGACATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAA
T  D  I  R  L  Q  M  P  R  K  K  K  D  E  Y  F  E  L  Y  E

GCATCTGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
A  S  V  A  R  Y  S  D  L  P  E  K  A  N  *
(SEQ ID NOs: 05 & 06)
```

Figure 5A

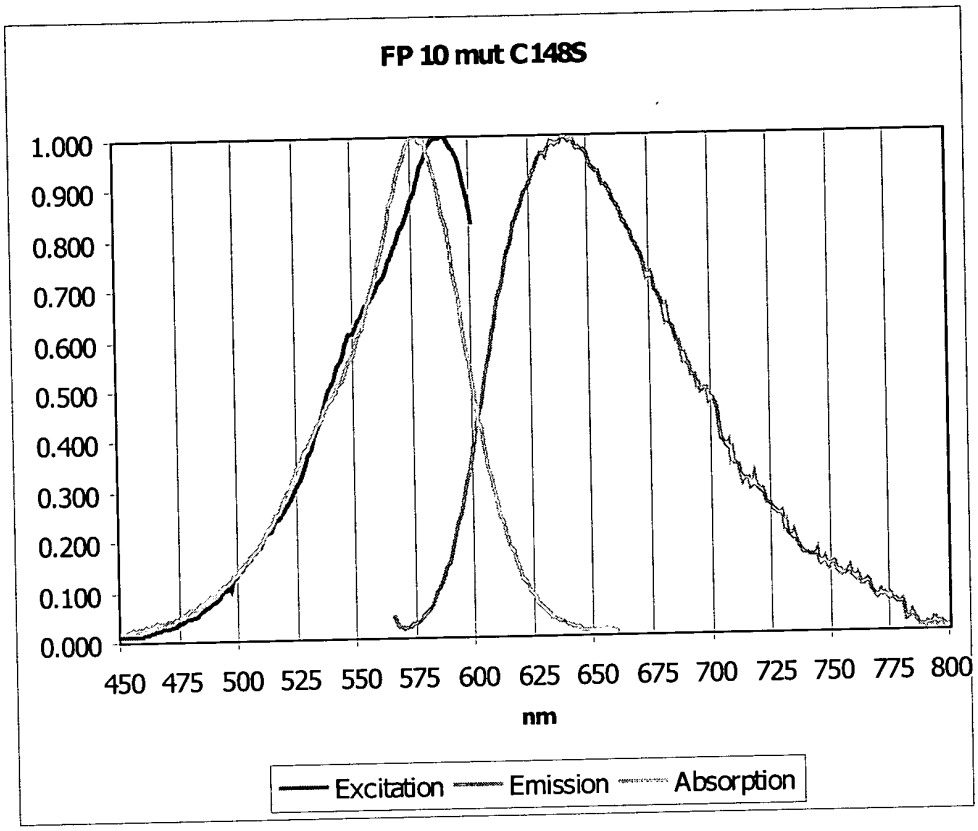

Figure 5B

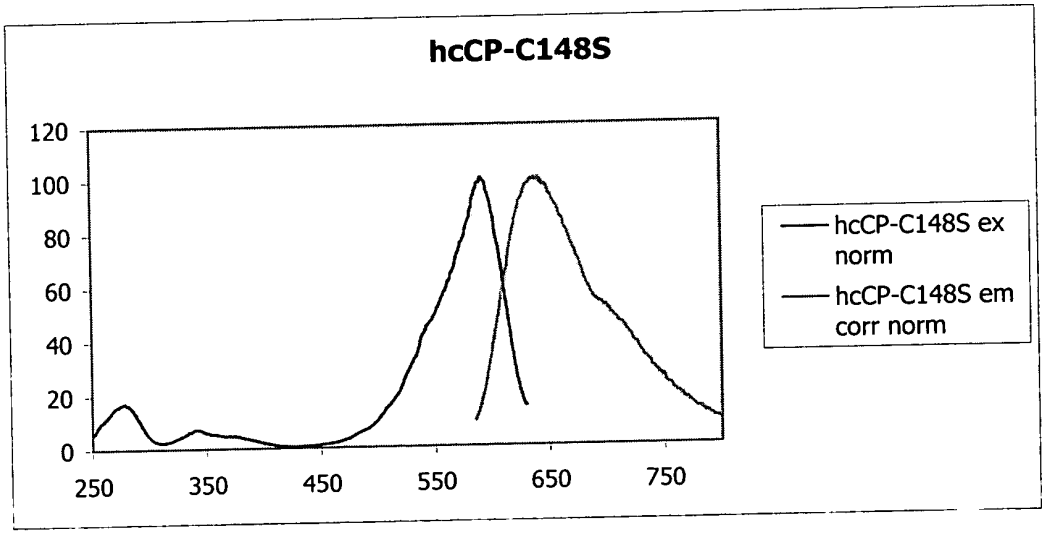

Figure 6

Heteractis crispa fluorescent protein **mutant 44-9**

point mutations: numbering **A5S,T39A,C148S,L181H,P208L,K211E** according to GFP numbering

A2S,T36A,C143S,L173H,P201L,K204E according to self-numbering.

```
                    80        90       100       110       120
                     TCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATGTACAT
                     S  G  L  L  K  E  S  M  R  I  K  M  Y  M

         130       140       150       160       170       180
GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
 E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N  P  F

         190       200       210       220       230       240
TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
 A  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F  A  F

         250       260       270       280       290       300
CGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
 D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T  A  E

         310       320       330       340       350       360
GATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
 I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T  T  T

         370       380       390       400       410       420
CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
 Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N  C  L

         430       440       450       460       470       480
TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
 I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M  K  N

         490       500       510       520       530       540
CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCCTGTG
 K  S  G  G  W  E  P  S  T  E  V  V  Y  P  E  N  G  V  L  C

         550       560       570       580       590       600
TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC
 G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  H  Y  T

         610       620       630       640       650       660
TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA
 S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F  T  D

         670       680       690       700       710       720
CATCCGCCTTCAGATGCTGAGGAAAGAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
 I  R  L  Q  M  L  R  K  E  K  D  E  Y  F  E  L  Y  E  A  S

         730       740       750       760
TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
 V  A  R  Y  S  D  L  P  E  K  A  N  *   (SEQ ID NOs: 07 & 08)
```

Figure 7A

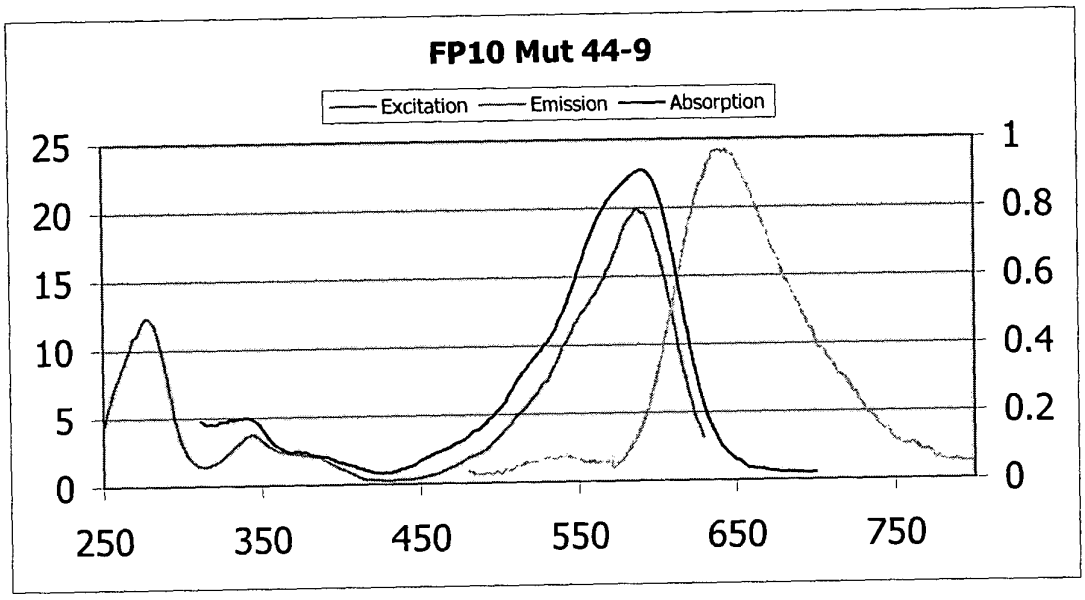

Figure 7B

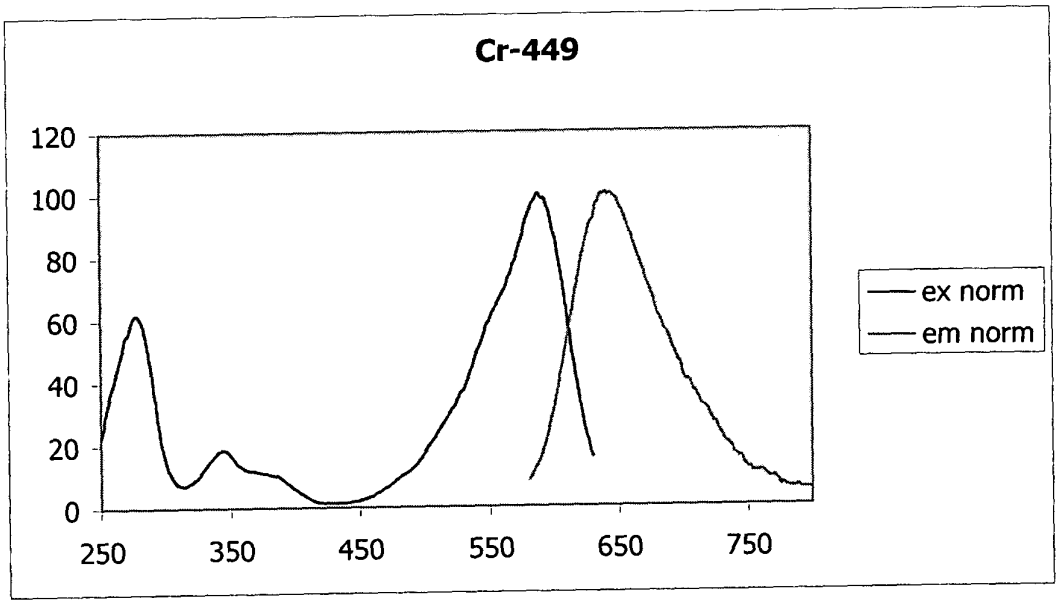

Figure 8

Crispa 44-6 mutant possesses six amino acid substitutions vs. wild type:
A2S,T36A,A65E,C143S,L173H,P201L.

```
                              TCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATGTACAT
                              S  G  L  L  K  E  S  M  R  I  K  M  Y  M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
 E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N  P  F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
 A  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F  A  F

CGACATTTTGGCACCGTGTTGTGCGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
 D  I  L  A  P  C  C  A  Y  G  S  R  T  F  V  H  H  T  A  E

GATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
 I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T  T  T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
 Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N  C  L

TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
 I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M  K  N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCCTGTG
 K  S  G  G  W  E  P  S  T  E  V  V  Y  P  E  N  G  V  L  C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC
 G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  H  Y  T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA
 S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F  T  D

CATCCGCCTTCAGATGCTGAGGAAAGAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
 I  R  L  Q  M  L  R  K  E  K  D  E  Y  F  E  L  Y  E  A  S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
 V  A  R  Y  S  D  L  P  E  K  A  N  *
```

(SEQ ID NO: 09 & 10)

Figure 9

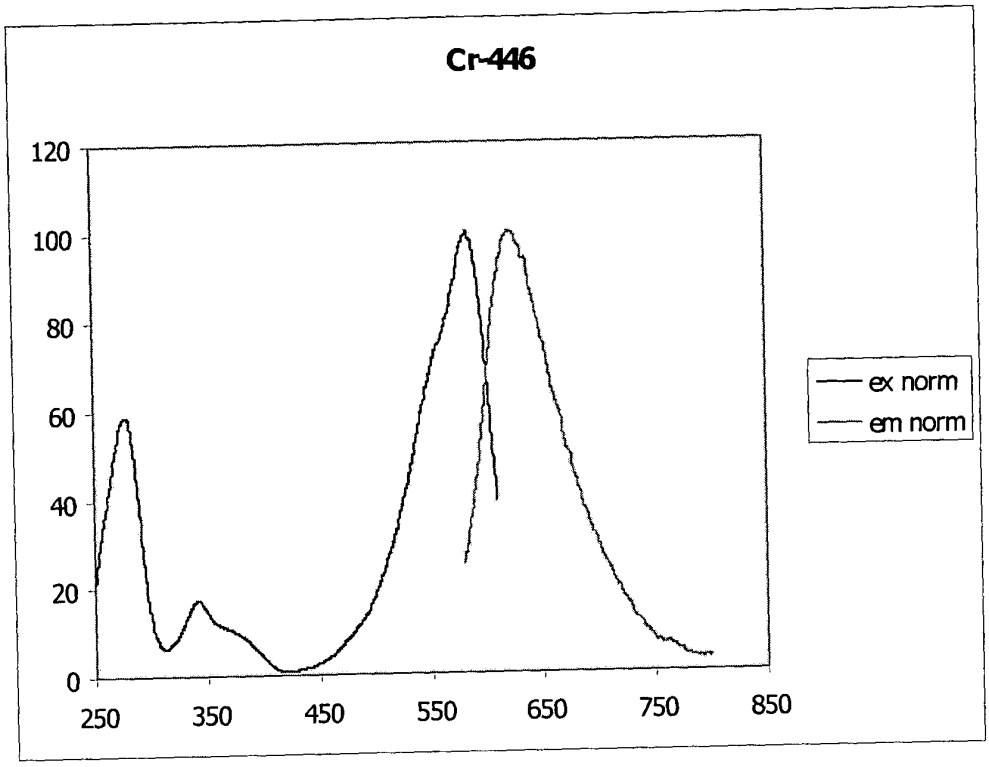

Figure 10

The amino acid sequence of FP10-cr1 is:

M S G L L K E S M R I K M Y M E G T V N G H Y
F K C E G E G D G N P F A G T Q S M R I H V T
E G A P L P F A F D I L A P C C E Y G S R T F
V H H T A E I P D F F K Q S F P E G F T W E R
T T T Y E D G G I L T A H Q D T S L E G N C L
I Y K V K V H G T N F P A D G P V M K N K S G
G W E P S T E V V Y P E N G V L C G R N V M A
L K V G D R R L I C H H Y T S Y R S K K A V R
A L T M P G F H F T D I R L Q M L R K E K D E
Y F E L Y E A S V A R Y S D L P E K A N (SEQ ID NO:12)

A "humanized" nt sequence encoding the above cr-1 mutant is:

ATGGTGAGCGGCCTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCAC
TACTTCAAGTGCGAGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAGCATGAGAATCCACGTG
ACCGAGGGCGCCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACC
TTCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAG
AGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCAGGACACCAGCCTGGAGGGCAACTGC
CTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGC
GGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATG
GCCCTGAAGGTGGGCGACCGGCACCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTG
CGCGCCCTGACCATGCCCGGCTTCCACTTCACCGACATCCGGCTCCAGATGCTGCGGAAGAAGAAGGAC
GAGTACTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCGACCTGCCCGAGAAGGCCAACTGA
(SEQ ID NO:11)

Alternative cr1 amino acid sequence

MSGLLKESMRIKMYMEGTVNGHYFKCEGEGDGNPFAGTQSMRIHVTEGAPLPFAFDILAPCCEYGSRTF
VHHTAEIPDFFKQSFPEGFTWERTTTYEDGGILTAHQDTSLEGNCLIYKVKVHGTNFPADGPVMKNKSG
GWEPSTEVVYPENGVLCGRNVMALKVGDRRLICHHYTSYRSKKAVRALTMPGFHFTDIRLQMLRKEKDE
YFELYEASVARYSDLPEKAN* SEQ ID NO:14)

Amino acid sequence encoding above alternative sequence:

ATGGTGAGCGGCCTGCTGAAGGAGAGCATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCAC
TACTTCAAGTGCGAGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAGCATGCGGATCCACGTG
ACCGAGGGCGCCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACC
TTCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAG
AGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCAGGACACCAGCCTGGAGGGCAACTGC
CTGATCTACAAGGTGAAGGTGCTGGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGC
GGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATG
GCCCTGAAGGTGGGCGACCGGCGGCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTG
CGGGCCCTGACCATGCCCGGCTTCCACTTCACCGACATCCGGCTGCAGATGCTGCGGAAGGAGAAGGAC
GAGTACTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCGACCTGCCCGAGAAGGCCAACTGA
(SEQ ID NO:13)

Figure 11

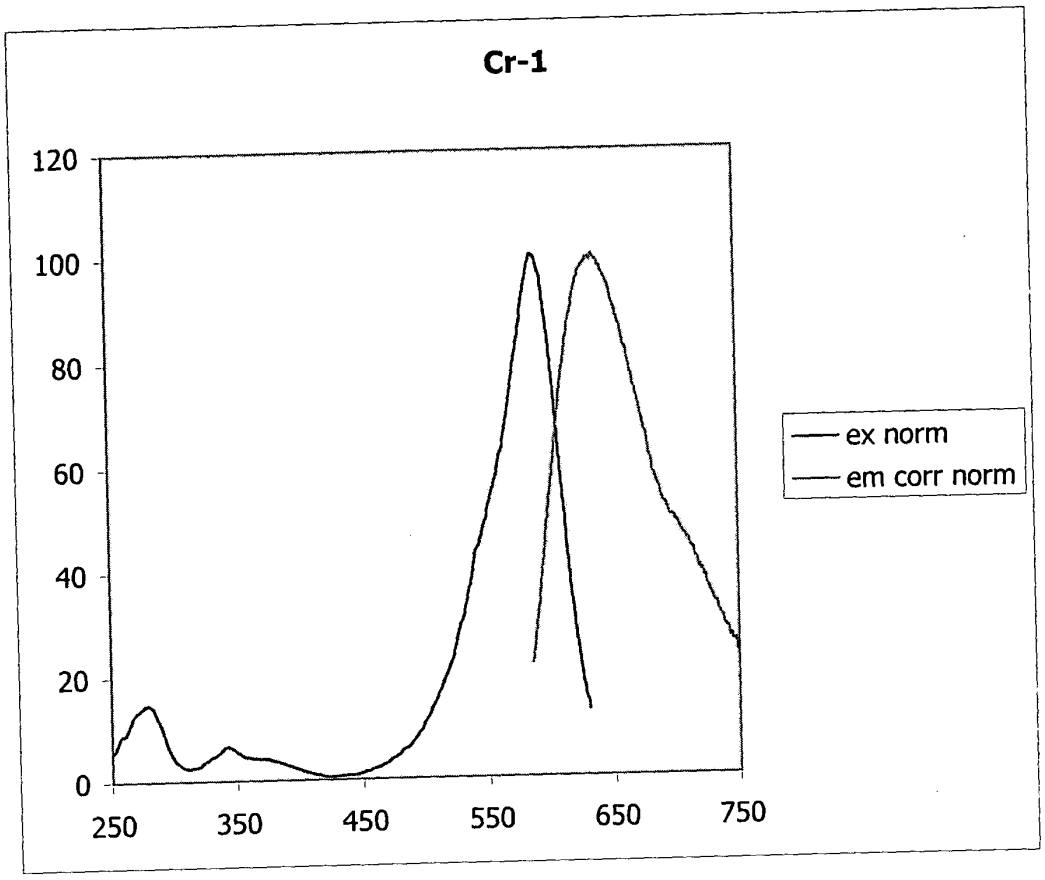
Cr-1
120
100
80
60
40
20
0
250
350
450
550
650
750
ex norm
em corr norm

FIGURE 12

Cr-449-tandem (4-amino acid linker between monomers is in double underline).

```
   1    A CCG GTC GCC ACC ATG GTG AGC GGC CTG CTG AAG GAG AGC ATG CGC      46
   1      AgeI              M   V   S   G   L   L   K   E   S   M   R      11

  47  ATC AAG ATG TAC ATG GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC      94
  12    I   K   M   Y   M   E   G   T   V   N   G   H   Y   F   K   C      27

  95  GAG GGC GAG GGC GAC GGC AAC CCC TTC GCC GGC ACC CAG AGC ATG CGG     142
  28    E   G   E   G   D   G   N   P   F   A   G   T   Q   S   M   R      43

 143  ATC CAC GTG ACC GAG GGC GCC CCC CTG CCC TTC GCC TTC GAC ATC CTG     190
  44    I   H   V   T   E   G   A   P   L   P   F   A   F   D   I   L      59

 191  GCC CCC TGC TGC GAG TAC GGC AGC AGG ACC TTC GTG CAC CAC ACC GCC     238
  60    A   P   C   C   E   Y   G   S   R   T   F   V   H   H   T   A      75

 239  GAG ATC CCC GAC TTC TTC AAG CAG AGC TTC CCC GAG GGC TTC ACC TGG     286
  76    E   I   P   D   F   F   K   Q   S   F   P   E   G   F   T   W      91

 287  GAG AGA ACC ACC ACC TAC GAG GAC GGC GGC ATC CTG ACC GCC CAC CAG     334
  92    E   R   T   T   T   Y   E   D   G   G   I   L   T   A   H   Q     107

 335  GAC ACC AGC CTG GAG GGC AAC TGC CTG ATC TAC AAG GTG AAG GTG CTG     382
 108    D   T   S   L   E   G   N   C   L   I   Y   K   V   K   V   L     123

 383  GGC ACC AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAC AAG AGC GGC     430
 124    G   T   N   F   P   A   D   G   P   V   M   K   N   K   S   G     139

 431  GGC TGG GAG CCC AGC ACC GAG GTG GTG TAC CCC GAG AAC GGC GTG CTG     478
 140    G   W   E   P   S   T   E   V   V   Y   P   E   N   G   V   L     155

 479  TGC GGC CGG AAC GTG ATG GCC CTG AAG GTG GGC GAC CGG CGG CTG ATC     526
 156    C   G   R   N   V   M   A   L   K   V   G   D   R   R   L   I     171

 527  TGC CAC CAC TAC ACC AGC TAC CGG AGC AAG AAG GCC GTG CGG GCC CTG     574
 172    C   H   H   Y   T   S   Y   R   S   K   K   A   V   R   A   L     187

 575  ACC ATG CCC GGC TTC CAC TTC ACC GAC ATC CGG CTG CAG ATG CTG CGG     622
 188    T   M   P   G   F   H   F   T   D   I   R   L   Q   M   L   R     203

 623  AAG GAG AAG GAC GAG TAC TTC GAG CTG TAC GAG GCC AGC GTG GCC CGG     670
 204    K   E   K   D   E   Y   F   E   L   Y   E   A   S   V   A   R     219

 671  TAC AGC GAC CTG CCC GAG AAG GCC AAC AGA TCT CCC GGG ATG GTG AGC     718
 220    Y   S   D   L   P   E   K   A   N   R   S   P   G   M   V   S     235

 719  GGC CTG CTG AAG GAG AGC ATG CGC ATC AAG ATG TAC ATG GAG GGC ACC     766
 236    G   L   L   K   E   S   M   R   I   K   M   Y   M   E   G   T     251

 767  GTG AAC GGC CAC TAC TTC AAG TGC GAG GGC GAG GGC GAC GGC AAC CCC     814
 252    V   N   G   H   Y   F   K   C   E   G   E   G   D   G   N   P     267

 815  TTC GCC GGC ACC CAG AGC ATG CGG ATC CAC GTG ACC GAG GGC GCC CCC     862
 268    F   A   G   T   Q   S   M   R   I   H   V   T   E   G   A   P     283

 863  CTG CCC TTC GCC TTC GAC ATC CTG GCC CCC TGC TGC GAG TAC GGC AGC     910
 284    L   P   F   A   F   D   I   L   A   P   C   C   E   Y   G   S     299
```

Figure 12 (continued)

```
 911  AGG ACC TTC GTG CAC CAC ACC GCC GAG ATC CCC GAC TTC TTC AAG CAG   958
 300   R   T   F   V   H   H   T   A   E   I   P   D   F   F   K   Q    315

 959  AGC TTC CCC GAG GGC TTC ACC TGG GAG AGA ACC ACC ACC TAC GAG GAC  1006
 316   S   F   P   E   G   F   T   W   E   R   T   T   T   Y   E   D    331

1007  GGC GGC ATC CTG ACC GCC CAC CAG GAC ACC AGC CTG GAG GGC AAC TGC  1054
 332   G   G   I   L   T   A   H   Q   D   T   S   L   E   G   N   C    347

1055  CTG ATC TAC AAG GTG AAG GTG CTG GGC ACC AAC TTC CCC GCC GAC GGC  1102
 348   L   I   Y   K   V   K   V   L   G   T   N   F   P   A   D   G    363

1103  CCC GTG ATG AAG AAC AAG AGC GGC GGC TGG GAG CCC AGC ACC GAG GTG  1150
 364   P   V   M   K   N   K   S   G   G   W   E   P   S   T   E   V    379

1151  GTG TAC CCC GAG AAC GGC GTG CTG TGC GGC CGG AAC GTG ATG GCC CTG  1198
 380   V   Y   P   E   N   G   V   L   C   G   R   N   V   M   A   L    395

1199  AAG GTG GGC GAC CGG CGG CTG ATC TGC CAC CAC TAC ACC AGC TAC CGG  1246
 396   K   V   G   D   R   R   L   I   C   H   H   Y   T   S   Y   R    411

1247  AGC AAG AAG GCC GTG CGG GCC CTG ACC ATG CCC GGC TTC CAC TTC ACC  1294
 412   S   K   K   A   V   R   A   L   T   M   P   G   F   H   F   T    427

1295  GAC ATC CGG CTG CAG ATG CTG CGG AAG GAG AAG GAC GAG TAC TTC GAG  1342
 428   D   I   R   L   Q   M   L   R   K   E   K   D   E   Y   F   E    443

1343  CTG TAC GAG GCC AGC GTG GCC CGG TAC AGC GAC CTG CCC GAG AAG GCC  1390
 444   L   Y   E   A   S   V   A   R   Y   S   D   L   P   E   K   A    459

1391  AAC TGA
 460   N   *
```

(SEQ ID NOS. 15 & 16)

Figure 13

Cr-449-tandem-actin (4-amino acid linker between Cr-449 monomers is noted in double underline; 4-amino acid linker between second Cr-449 and actin is noted in dashed underline).

```
  1   A CCG GTC GCC ACC ATG GTG AGC GGC CTG CTG AAG GAG AGC ATG CGC    46
  1     AgeI              M   V   S   G   L   L   K   E   S   M   R    11

 47  ATC AAG ATG TAC ATG GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC   94
 12   I   K   M   Y   M   E   G   T   V   N   G   H   Y   F   K   C    27

 95  GAG GGC GAG GGC GAC GGC AAC CCC TTC GCC GGC ACC CAG AGC ATG CGG  142
 28   E   G   E   G   D   G   N   P   F   A   G   T   Q   S   M   R    43

143  ATC CAC GTG ACC GAG GGC GCC CCC CTG CCC TTC GCC TTC GAC ATC CTG  190
 44   I   H   V   T   E   G   A   P   L   P   F   A   F   D   I   L    59

191  GCC CCC TGC TGC GAG TAC GGC AGC AGG ACC TTC GTG CAC CAC ACC GCC  238
 60   A   P   C   C   E   Y   G   S   R   T   F   V   H   H   T   A    75

239  GAG ATC CCC GAC TTC TTC AAG CAG AGC TTC CCC GAG GGC TTC ACC TGG  286
 76   E   I   P   D   F   F   K   Q   S   F   P   E   G   F   T   W    91

287  GAG AGA ACC ACC ACC TAC GAG GAC GGC GGC ATC CTG ACC GCC CAC CAG  334
 92   E   R   T   T   T   Y   E   D   G   G   I   L   T   A   H   Q   107

335  GAC ACC AGC CTG GAG GGC AAC TGC CTG ATC TAC AAG GTG AAG GTG CTG  382
108   D   T   S   L   E   G   N   C   L   I   Y   K   V   K   V   L   123

383  GGC ACC AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAC AAG AGC GGC  430
124   G   T   N   F   P   A   D   G   P   V   M   K   N   K   S   G   139

431  GGC TGG GAG CCC AGC ACC GAG GTG GTG TAC CCC GAG AAC GGC GTG CTG  478
140   G   W   E   P   S   T   E   V   V   Y   P   E   N   G   V   L   155

479  TGC GGC CGG AAC GTG ATG GCC CTG AAG GTG GGC GAC CGG CGG CTG ATC  526
156   C   G   R   N   V   M   A   L   K   V   G   D   R   R   L   I   171

527  TGC CAC CAC TAC ACC AGC TAC CGG AGC AAG AAG GCC GTG CGG GCC CTG  574
172   C   H   H   Y   T   S   Y   R   S   K   K   A   V   R   A   L   187

575  ACC ATG CCC GGC TTC CAC TTC ACC GAC ATC CGG CTG CAG ATG CTG CGG  622
188   T   M   P   G   F   H   F   T   D   I   R   L   Q   M   L   R   203

623  AAG GAG AAG GAC GAG TAC TTC GAG CTG TAC GAG GCC AGC GTG GCC CGG  670
204   K   E   K   D   E   Y   F   E   L   Y   E   A   S   V   A   R   219

671  TAC AGC GAC CTG CCC GAG AAG GCC AAC AGA TCT CCC GGG ATG GTG AGC  718
220   Y   S   D   L   P   E   K   A   N   R   S   P   G   M   V   S   235

719  GGC CTG CTG AAG GAG AGC ATG CGC ATC AAG ATG TAC ATG GAG GGC ACC  766
236   G   L   L   K   E   S   M   R   I   K   M   Y   M   E   G   T   251

767  GTG AAC GGC CAC TAC TTC AAG TGC GAG GGC GAG GGC GAC GGC AAC CCC  814
252   V   N   G   H   Y   F   K   C   E   G   E   G   D   G   N   P   267

815  TTC GCC GGC ACC CAG AGC ATG CGG ATC CAC GTG ACC GAG GGC GCC CCC  862
268   F   A   G   T   Q   S   M   R   I   H   V   T   E   G   A   P   283
```

Figure 13 (continued)

```
863  CTG CCC TTC GCC TTC GAC ATC CTG GCC CCC TGC TGC GAG TAC GGC AGC   910
284   L   P   F   A   F   D   I   L   A   P   C   C   E   Y   G   S   299

911  AGG ACC TTC GTG CAC CAC ACC GCC GAG ATC CCC GAC TTC TTC AAG CAG   958
300   R   T   F   V   H   H   T   A   E   I   P   D   F   F   K   Q   315

959  AGC TTC CCC GAG GGC TTC ACC TGG GAG AGA ACC ACC ACC TAC GAG GAC  1006
316   S   F   P   E   G   F   T   W   E   R   T   T   T   Y   E   D   331

1007 GGC GGC ATC CTG ACC GCC CAC CAG GAC ACC AGC CTG GAG GGC AAC TGC  1054
332   G   G   I   L   T   A   H   Q   D   T   S   L   E   G   N   C   347

1055 CTG ATC TAC AAG GTG AAG GTG CTG GGC ACC AAC TTC CCC GCC GAC GGC  1102
348   L   I   Y   K   V   K   V   L   G   T   N   F   P   A   D   G   363

1103 CCC GTG ATG AAG AAC AAG AGC GGC GGC TGG GAG CCC AGC ACC GAG GTG  1150
364   P   V   M   K   N   K   S   G   G   W   E   P   S   T   E   V   379

1151 GTG TAC CCC GAG AAC GGC GTG CTG TGC GGC CGG AAC GTG ATG GCC CTG  1198
380   V   Y   P   E   N   G   V   L   C   G   R   N   V   M   A   L   395

1199 AAG GTG GGC GAC CGG CGG CTG ATC TGC CAC CAC TAC ACC AGC TAC CGG  1246
396   K   V   G   D   R   R   L   I   C   H   H   Y   T   S   Y   R   411

1247 AGC AAG AAG GCC GTG CGG GCC CTG ACC ATG CCC GGC TTC CAC TTC ACC  1294
412   S   K   K   A   V   R   A   L   T   M   P   G   F   H   F   T   427

1295 GAC ATC CGG CTG CAG ATG CTG CGG AAG GAG AAG GAC GAG TAC TTC GAG  1342
428   D   I   R   L   Q   M   L   R   K   E   K   D   E   Y   F   E   443

1343 CTG TAC GAG GCC AGC GTG GCC CGG TAC AGC GAC CTG CCC GAG AAG GCC  1390
444   L   Y   E   A   S   V   A   R   Y   S   D   L   P   E   K   A   459

1391 AAC AGA ACT CGA GCT ATG GAT GAT GAT ATC GCC G...                 1424
460   N   R   T   R   A   M   D   D   D   I   A...                   470
                          actin
```

(SEQ ID NOs. 17 & 18).

Figure 14

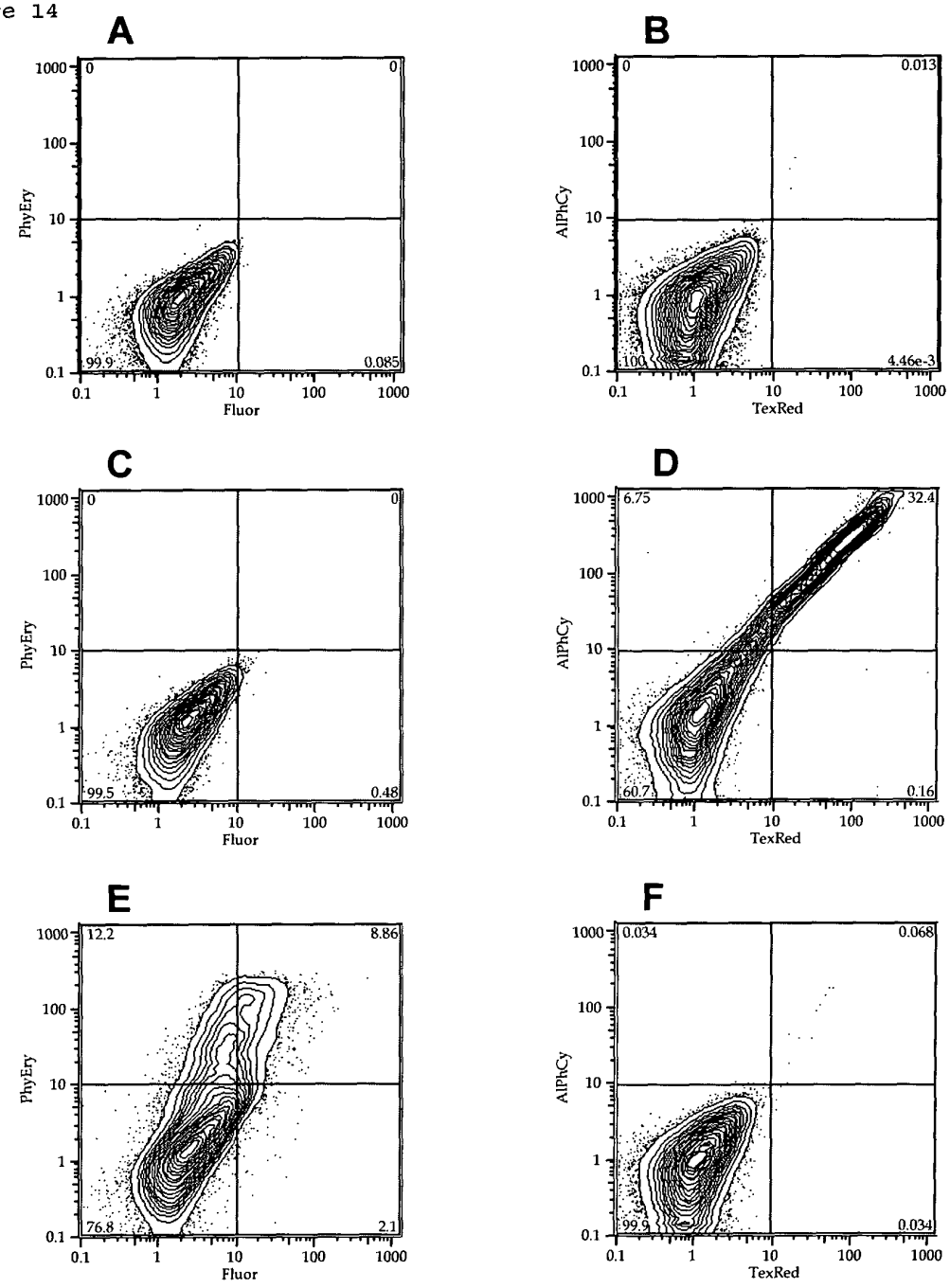
A
B
C
D
E
F
PhyEry
AlPhCy
Fluor
TexRed
0
0.013
0.085
4.46e-3
99.9
100
0.48
99.5
6.75
32.4
60.7
0.16
12.2
8.86
76.8
2.1
0.034
0.068
99.9
0.034
0.1
1
10
100
1000

Figure 15

Heteractis crispa chromoprotein hcCP mut C148S

C148S according to GFP numbering
C143S according to self-numbering.

```
                          ATGGCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATGTACAT
                          M  A  G  L  L  K  E  S  M  R  I  K  M  Y  M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
 E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N  P  F

TACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
 T  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F  A  F

CGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
 D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T  A  E

GATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
 I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T  T  T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
 Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N  C  L

TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
 I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M  K  N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCCTGTG
 K  S  G  G  W  E  P  S  T  E  V  V  Y  P  E  N  G  V  L  C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTCTATAC
 G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  L  Y  T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA
 S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F  T  D

CATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
 I  R  L  Q  M  P  R  K  K  K  D  E  Y  F  E  L  Y  E  A  S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
 V  A  R  Y  S  D  L  P  E  K  A  N  *
 SEQ ID NO:23 & 24
```

Figure 16

Crispa 44-6 mutant possesses six amino acid substitutions vs. wild type: A2S,T36A,A65E,C143S,L173H,P201L.

```
                         TCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATGTACAT
                          S  G  L  L  K  E  S  M  R  I  K  M  Y  M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
 E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N  P  F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
 A  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F  A  F

CGACATTTTGGCACCGTGTTGTGCGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
 D  I  L  A  P  C  C  A  Y  G  S  R  T  F  V  H  H  T  A  E

GATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
 I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T  T  T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
 Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N  C  L

                                         <---------
TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
 I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M  K  N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCCTGTG
 K  S  G  G  W  E  P  S  T  E  V  V  Y  P  E  N  G  V  L  C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC
 G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  H  Y  T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA
 S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F  T  D

CATCCGCCTTCAGATGCTGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
 I  R  L  Q  M  L  R  K  K  K  D  E  Y  F  E  L  Y  E  A  S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
 V  A  R  Y  S  D  L  P  E  K  A  N  *
SEQ ID NO:25 & 26
```

Figure 17

Heteractis crispa chromoprotein **wild type (base isoform)**

```
        10        20        30        40        50        60
5'ACCATTTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGAACGAAAACTGACCCAAATTACA
        70        80        90       100       110       120
  TCTTCCTCCTGGATCCTTACCATGGCTGGTTTGTTGAAAGAAAGTATGCGCATCAAGATG
                          M  A  G  L  L  K  E  S  M  R  I  K  M
       130       140       150       160       170       180
  TACATGGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAAC
  Y  M  E  G  T  V  N  G  H  Y  F  K  C  E  G  E  G  D  G  N
       190       200       210       220       230       240
  CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTT
  P  F  T  G  T  Q  S  M  R  I  H  V  T  E  G  A  P  L  P  F
       250       260       270       280       290       300
  GCCTTCGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACG
  A  F  D  I  L  A  P  C  C  E  Y  G  S  R  T  F  V  H  H  T
       310       320       330       340       350       360
  GCAGAGATTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACC
  A  E  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  T
       370       380       390       400       410       420
  ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC
  T  T  Y  E  D  G  G  I  L  T  A  H  Q  D  T  S  L  E  G  N
       430       440       450       460       470       480
  TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATG
  C  L  I  Y  K  V  K  V  L  G  T  N  F  P  A  D  G  P  V  M
       490       500       510       520       530       540
  AAGAACAAATCAGGAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGAGAATGGTGTC
  K  N  K  S  G  G  W  E  P  C  T  E  V  V  Y  P  E  N  G  V
       550       560       570       580       590       600
  CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC
  L  C  G  R  N  V  M  A  L  K  V  G  D  R  R  L  I  C  H  L
       610       620       630       640       650       660
  TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTT
  Y  T  S  Y  R  S  K  K  A  V  R  A  L  T  M  P  G  F  H  F
       670       680       690       700       710       720
  ACAGACATCCGCCTTCAGATGCCGAGGAAAACGAAAGACGAGTACTTTGAACTGTACGAA
  T  D  I  R  L  Q  M  P  R  K  T  K  D  E  Y  F  E  L  Y  E
       730       740       750       760       770       780
  GCATCTGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGATTGTTCCCAGTGACA
  A  S  V  A  R  Y  S  D  L  P  E  K  A  N  *
       790       800       810       820       830       840
  CCAGACTGCTGTCAGCTTTTGGTTAAAGCCCGAAAGACAAAAGGACATTTGTAGTTTAGT
       850       860       870       880       890       900
  TTATATTTCCCTTTCATTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAAATGCTC
       910
  CATTAAACCT 3'  (SEQ ID NOs: 27 & 28)
```